

SEQUENCE LISTING

<110> Presnell, Scott R.
Xu, Wenfeng
Novak, Julia E.
Whitmore, Theodore E.
Grant, Francis J.

<120> CYTOKINE RECEPTOR ZCYTOR19

<130> 00-108

<150> US 60/253,561
<151> 2000-11-28

<150> US 60/267,211
<151> 2001-02-07

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<170> FastSEQ for Windows Version 3.0

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<212> DNA
<213> Homo sapiens

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Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
1 5 10 15

48

gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
20 25 30

96

ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc

144

Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly				
35	40	45		
aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc				192
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr				
50	55	60		
cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg				240
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu				
65	70	75	80	
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc				288
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe				
85	90	95		
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg				336
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val				
100	105	110		
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct				384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro				
115	120	125		
gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg				432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr				
130	135	140		
tac cag ctg ccc ccc tgc atg ccc cca ctg ttt ctg aag tat gag gtg				480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val				
145	150	155	160	
gca ttt tgg ggg ggg gcc gga acc aag acc cta ttt cca gtc act				528
Ala Phe Trp Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr				
165	170	175		
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa				576
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu				
180	185	190		
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa				624
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys				
195	200	205		

tac	agc	aag	ttc	tct	aag	ccc	acc	tgc	ttc	ttg	ctg	gag	gtc	cca	gaa	672
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu	
210			215							220						
gcc	aac	tgg	gct	ttc	ctg	gtg	ctg	cca	tcg	ctt	ctg	ata	ctg	ctg	tta	720
Ala	Asn	Trp	Ala	Phe	Leu	Val	Leu	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	
225			230							235				240		
gta	att	gcc	gca	ggg	ggt	gtg	atc	tgg	aag	acc	ctc	atg	ggg	aac	ccc	768
Val	Ile	Ala	Ala	Gly	Gly	Val	Ile	Trp	Lys	Thr	Leu	Met	Gly	Asn	Pro	
245			250							255						
tgg	ttt	cag	cgg	gca	aag	atg	cca	cgg	gcc	ctg	gaa	ctg	acc	aga	ggg	816
Trp	Phe	Gln	Arg	Ala	Lys	Met	Pro	Arg	Ala	Leu	Glu	Leu	Thr	Arg	Gly	
260			265							270						
gtc	agg	ccg	acg	cct	cga	gtc	agg	gcc	cca	gcc	acc	caa	cag	aca	aga	864
Val	Arg	Pro	Thr	Pro	Arg	Val	Arg	Ala	Pro	Ala	Thr	Gln	Gln	Thr	Arg	
275			280							285						
tgg	aag	aag	gac	ctt	gca	gag	gac	gaa	gag	gag	gat	gag	gag	gac	912	
Trp	Lys	Lys	Asp	Leu	Ala	Glu	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Asp		
290			295							300						
aca	gaa	gat	ggc	gtc	agc	ttc	cag	ccc	tac	att	gaa	cca	cct	tct	ttc	960
Thr	Glu	Asp	Gly	Val	Ser	Phe	Gln	Pro	Tyr	Ile	Glu	Pro	Pro	Ser	Phe	
305			310							315			320			
ctg	ggg	caa	gag	cac	cag	gct	cca	ggg	cac	tcg	gag	gct	ggt	ggg	gtg	1008
Leu	Gly	Gln	Glu	His	Gln	Ala	Pro	Gly	His	Ser	Glu	Ala	Gly	Gly	Val	
325			330							335						
gac	tca	ggg	agg	ccc	agg	gct	cct	ctg	gtc	cca	agc	gaa	ggc	tcc	tct	1056
Asp	Ser	Gly	Arg	Pro	Arg	Ala	Pro	Leu	Val	Pro	Ser	Glu	Gly	Ser	Ser	
340			345							350						
gct	tgg	gat	tct	tca	gac	aga	agc	tgg	gcc	agc	act	gtg	gac	tcc	tcc	1104
Ala	Trp	Asp	Ser	Ser	Asp	Arg	Ser	Trp	Ala	Ser	Thr	Val	Asp	Ser	Ser	
355			360							365						
tgg	gac	agg	gct	ggg	tcc	tct	ggc	tat	ttg	gct	gag	aag	ggg	cca	ggc	1152
Trp	Asp	Arg	Ala	Gly	Ser	Ser	Gly	Tyr	Leu	Ala	Glu	Lys	Gly	Pro	Gly	
370			375							380						

caa	ggg	ccg	ggt	ggg	gat	ggg	caa	gaa	tct	ctc	cca	cca	cct	gaa	1200	
Gln	Gly	Pro	Gly	Gly	Asp	Gly	His	Gln	Glu	Ser	Leu	Pro	Pro	Pro	Glu	
385	390							395						400		
ttc	tcc	aag	gac	tcg	ggt	ttc	ctg	gaa	gag	ctc	cca	gaa	gat	aac	ctc	1248
Phe	Ser	Lys	Asp	Ser	Gly	Phe	Leu	Glu	Glu	Leu	Pro	Glu	Asp	Asn	Leu	
405							410						415			
tcc	tcc	tgg	gcc	acc	tgg	ggc	acc	tta	cca	ccg	gag	ccg	aat	ctg	gtc	1296
Ser	Ser	Trp	Ala	Thr	Trp	Gly	Thr	Leu	Pro	Pro	Glu	Pro	Asn	Leu	Val	
420							425						430			
cct	ggg	gga	ccc	cca	gtt	tct	ctt	cag	aca	ctg	acc	ttc	tgc	tgg	gaa	1344
Pro	Gly	Gly	Pro	Pro	Val	Ser	Leu	Gln	Thr	Leu	Thr	Phe	Cys	Trp	Glu	
435							440						445			
agc	agc	cct	gag	gag	gaa	gag	gag	gcg	agg	gaa	tca	gaa	att	gag	gac	1392
Ser	Ser	Pro	Glu	Glu	Glu	Glu	Glu	Ala	Arg	Glu	Ser	Glu	Ile	Glu	Asp	
450							455						460			
agc	gat	gct	ggc	agc	tgg	ggg	gct	gag	agc	acc	cag	agg	acc	gag	gac	1440
Ser	Asp	Ala	Gly	Ser	Trp	Gly	Ala	Glu	Ser	Thr	Gln	Arg	Thr	Glu	Asp	
465							470						475			
agg	ggc	cg	aca	ttg	ggg	cat	tac	atg	gcc	agg	tga					1476
Arg	Gly	Arg	Thr	Leu	Gly	His	Tyr	Met	Ala	Arg						
485									490							

<210> 2
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 <212> PRT
 <213> Homo sapiens

<400> 2
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 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45

Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr
 165 170 175
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
 180 185 190
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
 195 200 205
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
 210 215 220
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu
 225 230 235 240
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
 245 250 255
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly
 260 265 270
 Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg
 275 280 285
 Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp
 290 295 300
 Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe
 305 310 315 320
 Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val
 325 330 335
 Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser
 340 345 350
 Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser
 355 360 365
 Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly
 370 375 380

Gln	Gly	Pro	Gly	Gly	Asp	Gly	His	Gln	Glu	Ser	Leu	Pro	Pro	Pro	Glu
385					390					395					400
Phe	Ser	Lys	Asp	Ser	Gly	Phe	Leu	Glu	Glu	Leu	Pro	Glu	Asp	Asn	Leu
						405				410					415
Ser	Ser	Trp	Ala	Thr	Trp	Gly	Thr	Leu	Pro	Pro	Glu	Pro	Asn	Leu	Val
							420			425					430
Pro	Gly	Gly	Pro	Pro	Val	Ser	Leu	Gln	Thr	Leu	Thr	Phe	Cys	Trp	Glu
							435		440			445			
Ser	Ser	Pro	Glu	Glu	Glu	Glu	Ala	Arg	Glu	Ser	Glu	Ile	Glu	Asp	
							450		455			460			
Ser	Asp	Ala	Gly	Ser	Trp	Gly	Ala	Glu	Ser	Thr	Gln	Arg	Thr	Glu	Asp
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Arg	Gly	Arg	Thr	Leu	Gly	His	Tyr	Met	Ala	Arg					
							485			490					

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<221> misc_feature
<222> (1)...(1473)
<223> n = A,T,C or G

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ytnacntggy tnccnggnyt nggnaayccn cargaygtna cntaytgyt ngcntaycar
wsnwsnccna cnmgnmgnmg ntggmngar gtngargart gygcnggnac naargarytn
ytnagywsna ttagtgyyt naaraarcar gaytntaya ayaarttyaa rggnmngntn
mgnacngtnw snccnwsnws naarwsnccn tgggtngarw sngartayyt ngaytayytn
tgygargtng arccngcncc nccngtntn gtnytnacnc aracngarga rathytnwsn
gcnaaygcna cntaycaryt nccnccntgy atgccnccny tntyytntaa rtaygargtn
gcnttytggg gngngngc nggnacnaar acnytnttgc cngtnacncc ncayggncar
ccngtnacra thacnytnca rccngcngcn wsngarcayc aytgyytnws ngcngnacn
athtayacnt tywsngtntcc naartaywsn aarttywsna arccnacntg ytttytntn
gargtnccng argcnaaytg ggcnttgyt gtnytnccnw snytntnat hytnytnytn
gtntathgcng cnngngngt nathtggaar acnytnatgg gnaayccntg gttycarmgn
gcnaaratgc cnmgnccnyt ngarytnacn mgngngntm gnccnacncc nmgngtmgn
gcncnccnacnca cncarcarac nmgnntggaar aargayytn gngargayga rgargargar

gaygargarg ayacngarga yggngtnwsn ttycarcnt ayathgarcc nccnwsntty	960
ytnggncarg arcaycargc nccngncay wsngargcng gnggngtnga ywsnggnmgn	1020
ccnmgngcnc cnytngtncc nwsngarggn wsnsngcnt gggaywsnws ngaymgnwsn	1080
tgggcnwsna cngtngayws nwsntggay mgngcnggnw snwsngnta yytngcngar	1140
aarggnccng gncarggncc nggngngay ggncaycarg arwsnytncc nccnccngar	1200
ttywsnaarg aywsngntt yytngargar ytnccngarg ayaayytnws nwsntggcn	1260
acntgggna cnytnccncc ngarccnaay ytngtnccng gngnccncc ngtnwsnytn	1320
caracnytna cnttytgytg ggarwsnwsn ccngargarg argargargc nmngarwsn	1380
garathgarg aywsngaygc ngnwsntgg ggngcngarw snacncarmg nacngargay	1440
mgnggnmgnna cnytnggnca ytayatggcn mgn	1473

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<212> PRT

<213> Homo sapiens

<400> 4

Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu Leu Ser Gln Asn	
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Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly Asn Pro Gln Asp	
20 25 30	
Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr Arg Arg Arg Trp	
35 40 45	
Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu Leu Cys Ser Met	
50 55 60	
Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe Lys Gly Arg Val	
65 70 75 80	
Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val Glu Ser Glu Tyr	
85 90 95	
Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro Val Leu Val Leu	
100 105 110	
Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr Tyr Gln Leu Pro	
115 120 125	
Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val Ala Phe Trp Gly	
130 135 140	
Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr Pro His Gly Gln	
145 150 155 160	
Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu His His Cys Leu	
165 170 175	
Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys Tyr Ser Lys Phe	
180 185 190	
Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro	
195 200	

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<223> WSXWS motif

<221> VARIANT
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<223> Xaa = Any Amino Acid

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<223> Oligonucleotide primer ZC21195

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23

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<212> DNA
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23

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<223> Oligonucleotide primer ZC14063

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Glu Tyr Met Pro Met Glu
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<210> 12
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<213> Artificial Sequence

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<223> FLAG peptide tag

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Asp Tyr Lys Asp Asp Asp Asp Lys
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<210> 13

<211> 699

<212> DNA

<213> Homo sapiens

<400> 13

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acccctgagg	tcacatgcgt	ggtgtggac	gtgagccacg	aagaccctga	ggtcaagttc	180
aacttgtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagcccg	ggaggagcag	240
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	300
ggcaaggagt	acaagtgcac	ggtctccaac	aaagccctcc	catcctccat	cgagaaaaacc	360
atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccg	420
gatgagctga	ccaaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatcccagc	480
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	540
cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agtcaccgt	ggacaagagc	600
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	660
tacacgcaga	agagcctctc	cctgtctccq	qgtaaataa			699

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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1 5 10 15

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ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser 35 40 45	144
ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser 50 55 60	192
ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc Leu Ser Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr 65 70 75 80	240
tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys 85 90 95	288
aaa gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys 100 105 110	336
cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro 115 120 125	384
aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys 130 135 140	432
gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp 145 150 155 160	480
tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu 165 170 175	528
gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu 180 185 190	576

cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac		624	
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn			
195	200	205	
aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg		672	
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly			
210	215	220	
cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag		720	
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu			
225	230	235	240
ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat		768	
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr			
245	250	255	
ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac		816	
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn			
260	265	270	
aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc		864	
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe			
275	280	285	
ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac		912	
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn			
290	295	300	
gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg		960	
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr			
305	310	315	320
cag aag agc ctc tcc ctg tct ccg ggt aaa		990	
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys			
325	330		
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 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 225 230 235 240
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
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 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

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<220>
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 <222> (1)...(321)

<400> 16

act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	cag	48	
Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln		
1		5						10					15				
ttg	aaa	tct	ggt	acc	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	ttc	tat	96	
Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	
								20					30				
ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	aac	gcc	ctc	caa	tcg	144	
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser		
								35					45				
ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	agc	aag	gac	agc	acc	192	
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr		
								50					60				
tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	gca	gac	tac	gag	aaa	240	
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys		
								65					75		80		
cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	ggc	ctg	agc	tcg	ccc	288	
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro		
								85					90		95		
gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag						321	
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	*							
								100					105				

<210> 17
 <211> 106
 <212> PRT

<213> Homo sapiens

<400> 17

Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln
1														15	
Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr
														30	
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser
														45	
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr
														60	
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys
														80	
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro
														95	
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys						
100															
105															

<210> 18

<211> 1563

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1563)

<400> 18

atg	gcg	ggg	ccc	gag	cgc	tgg	ggc	ccc	ctg	ctc	ctg	tgc	ctg	ctg	cag	48
Met	Ala	Gly	Pro	Glu	Arg	Trp	Gly	Pro	Leu	Leu	Leu	Cys	Leu	Leu	Gln	
1														15		

gcc	gct	cca	ggg	agg	ccc	cgt	ctg	gcc	cct	ccc	cag	aat	gtg	acg	ctg	96
Ala	Ala	Pro	Gly	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu	
														30		

ctc	tcc	cag	aac	ttc	agc	gtg	tac	ctg	aca	tgg	ctc	cca	ggg	ctt	ggc	144
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly	
35														45		

aac	ccc	cag	gat	gtg	acc	tat	ttt	gtg	gcc	tat	cag	agc	tct	ccc	acc	192
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr	
50														60		

CDS CDS CDS CDS CDS CDS CDS CDS CDS

cgt	aga	cgg	tgg	cgc	gaa	gtg	gaa	gag	tgt	gcg	gga	acc	aag	gag	ctg	240
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu	
65				70					75						80	
cta	tgt	tct	atg	atg	tgc	ctg	aag	aaa	cag	gac	ctg	tac	aac	aag	ttc	288
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe	
							85		90					95		
aag	gga	cgc	gtg	cgg	acg	gtt	tct	ccc	agc	tcc	aag	tcc	ccc	tgg	gtg	336
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val	
							100		105					110		
gag	tcc	gaa	tac	ctg	gat	tac	ctt	ttt	gaa	gtg	gag	ccg	gcc	cca	cct	384
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro	
							115		120					125		
gtc	ctg	gtg	ctc	acc	cag	acg	gag	atc	ctg	agt	gcc	aat	gcc	acg		432
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr	
							130		135					140		
tac	cag	ctg	ccc	ccc	tgc	atg	ccc	cca	ctg	gat	ctg	aag	tat	gag	gtg	480
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val	
							145		150					155		160
gca	ttc	tgg	aag	gag	ggg	gcc	gga	aac	aag	acc	cta	ttt	cca	gtc	act	528
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr	
											165		170		175	
ccc	cat	ggc	cag	cca	gtc	cag	atc	act	ctc	cag	cca	gct	gcc	agc	gaa	576
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu	
											180		185		190	
cac	cac	tgc	ctc	agt	gcc	aga	acc	atc	tac	acg	ttc	agt	gtc	ccg	aaa	624
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys	
											195		200		205	
tac	agc	aag	ttc	tct	aag	ccc	acc	tgc	ttc	ttg	ctg	gag	gtc	cca	gaa	672
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu	
											210		215		220	
gcc	aac	tgg	gct	ttc	ctg	gtg	ctg	cca	tcg	ctt	ctg	ata	ctg	ctg	tta	720

100 95 90 85 80 75 70 65 60 55 50 45 40 35 30 25 20 15 10 5 0

Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu				
225	230	235	240	
gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc				768
Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro				
245	250	255		
tgg ttt cag cgg gca aag atg cca cgg gcc ctg gac ttt tct gga cac				816
Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His				
260	265	270		
aca cac cct gtg gca acc ttt cag ccc agc aga cca gag tcc gtg aat				864
Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn				
275	280	285		
gac ttg ttc ctc tgt ccc caa aag gaa ctg acc aga ggg gtc agg ccg				912
Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro				
290	295	300		
acg cct cga gtc agg gcc cca gcc acc caa cag aca aga tgg aag aag				960
Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys				
305	310	315	320	
gac ctt gca gag gac gaa gag gag gag gat gag gag gac aca gaa gat				1008
Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp				
325	330	335		
ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc ctg ggg caa				1056
Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln				
340	345	350		
gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg gac tca ggg				1104
Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly				
355	360	365		
agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct gct tgg gat				1152
Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp				
370	375	380		
tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc tgg gac agg				1200
Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg				
385	390	395	400	

gct	ggg	tcc	tct	ggc	tat	ttg	gct	gag	aag	ggg	cca	ggc	caa	ggg	ccg		1248
Ala	Gly	Ser	Ser	Gly	Tyr	Leu	Ala	Glu	Lys	Gly	Pro	Gly	Gln	Gly	Pro		
							405				410				415		
ggt	ggg	gat	ggg	cac	caa	gaa	tct	ctc	cca	cca	cct	gaa	ttc	tcc	aag		1296
Gly	Gly	Asp	Gly	His	Gln	Glu	Ser	Leu	Pro	Pro	Pro	Glu	Phe	Ser	Lys		
							420				425				430		
gac	tcg	ggt	ttc	ctg	gaa	gag	ctc	cca	gaa	gat	aac	ctc	tcc	tcc	tgg		1344
Asp	Ser	Gly	Phe	Leu	Glu	Glu	Leu	Pro	Glu	Asp	Asn	Leu	Ser	Ser	Trp		
							435				440				445		
gcc	acc	tgg	ggc	acc	tta	cca	ccg	gag	ccg	aat	ctg	gtc	cct	ggg	gga		1392
Ala	Thr	Trp	Gly	Thr	Leu	Pro	Pro	Glu	Pro	Asn	Leu	Val	Pro	Gly	Gly		
							450				455				460		
ccc	cca	gtt	tct	ctt	cag	aca	ctg	acc	ttc	tgc	tgg	gaa	agc	agc	cct		1440
Pro	Pro	Val	Ser	Leu	Gln	Thr	Leu	Thr	Phe	Cys	Trp	Glu	Ser	Ser	Pro		
							465				470				475		
gag	gag	gaa	gag	gag	gct	agg	gaa	tca	gaa	att	gag	gac	agc	gat	gct		1488
Glu	Glu	Glu	Glu	Ala	Arg	Glu	Ser	Glu	Ile	Glu	Asp	Ser	Asp	Asp	Ala		
							485				490				495		
ggc	agc	tgg	ggg	gct	gag	agc	acc	cag	agg	acc	gag	gac	agg	ggc	cg		1536
Gly	Ser	Trp	Gly	Ala	Glu	Ser	Thr	Gln	Arg	Thr	Glu	Asp	Arg	Gly	Arg		
							500				505				510		
aca	ttg	ggg	cat	tac	atg	gcc	agg	tga									1563
Thr	Leu	Gly	His	Tyr	Met	Ala	Arg	*									
							515				520						

<210> 19

<211> 520

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln

1 5 10 15

Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu

20 25 30

DRAFT: 2009060600

Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
 165 170 175
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
 180 185 190
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
 195 200 205
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
 210 215 220
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu
 225 230 235 240
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
 245 250 255
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His
 260 265 270
 Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn
 275 280 285
 Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro
 290 295 300
 Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys
 305 310 315 320
 Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp
 325 330 335
 Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln
 340 345 350
 Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly
 355 360 365

Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp
 370 375 380
 Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg
 385 390 395 400
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
 405 410 415
 Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys
 420 425 430
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp
 435 440 445
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
 450 455 460
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480
 Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
 485 490 495
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
 500 505 510
 Thr Leu Gly His Tyr Met Ala Arg
 515 520

<210> 20
 <211> 674
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(633)

<400> 20
 atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag 48
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15

gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30

ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45

DRAFT: 2023-07-14 10:00:00

aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc	192
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr	
50 55 60	
cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg	240
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu	
65 70 75 80	
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc	288
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe	
85 90 95	
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg	336
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val	
100 105 110	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag cgg gcc cca cct	384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro	
115 120 125	
gtc ctg gtg ctc acc cag acg gag atc ctg agt gcc aat gcc acg	432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr	
130 135 140	
tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg	480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val	
145 150 155 160	
gca ttc tgg aag gag ggg gcc gga aac aag gtg gga agc tcc ttt cct	528
Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro	
165 170 175	
gcc ccc agg cta ggc ccg ctc ctc cac ccc ttc tta ctc agg ttc ttc	576
Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe	
180 185 190	
tca ccc tcc cag cct gct gca ccc ctc ctc cag gaa gtc ttc cct	624
Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro	
195 200 205	
gta cac tcc tgacttctgg cagtcagccc taataaaatc tgatcaaagt	673
Val His Ser	
210	

a

674

<210> 21
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 21
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro
 165 170 175
 Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe
 180 185 190
 Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro
 195 200 205
 Val His Ser
 210

<210> 22
 <211> 1422
 <212> DNA
 <213> Artificial Sequence

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<220>
 <223> Zcytor17-Fc4 fusion protein
 <221> CDS
 <222> (1)...(1422)

<400> 22

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gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc gag ttg aga cgc	96
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg	
20 25 30	
ttc cgt aga tcc agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg	144
Phe Arg Arg Ser Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu	
35 40 45	
ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc	192
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly	
50 55 60	
aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc	240
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr	
65 70 75 80	
cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg	288
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu	
85 90 95	
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc	336
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe	
100 105 110	
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg	384
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val	
115 120 125	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct	432
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro	
130 135 140	

gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg			480
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr			
145	150	155	160
tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg			528
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val			
165	170	175	
gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc act			576
Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr			
180	185	190	
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa			624
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu			
195	200	205	
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa			672
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys			
210	215	220	
tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa			720
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu			
225	230	235	240
gcc aac tgg aga tct tca gac aaa act cac aca tgc cca ccg tgc cca			768
Ala Asn Trp Arg Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro			
245	250	255	
gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc ccc cca aaa			816
Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys			
260	265	270	
ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg			864
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val			
275	280	285	
gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac			912
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr			
290	295	300	
gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag			960
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu			
305	310	315	320

cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac			1008
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His			
325	330	335	
cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa			1056
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys			
340	345	350	
gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc aaa ggg cag			1104
Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln			
355	360	365	
ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg			1152
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu			
370	375	380	
acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc			1200
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro			
385	390	395	400
agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac			1248
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn			
405	410	415	
tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc			1296
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu			
420	425	430	
tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc			1344
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val			
435	440	445	
ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag			1392
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln			
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<211> 473

<212> PRT

<213> Artificial Sequence

<400> 23

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							20		25					30	
Phe	Arg	Arg	Ser	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu
							35		40					45	
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly
							50		55					60	
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr
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Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu
							85		90					95	
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe
							100		105					110	
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
							115		120					125	
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
							130		135					140	
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr
							145		150		155			160	
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val
							165		170					175	
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr
							180		185					190	
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu
							195		200					205	
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys
							210		215					220	
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu
							225		230		235			240	
Ala	Asn	Trp	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
							245		250					255	
Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
							260		265					270	
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
							275		280					285	
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr
							290		295					300	

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 305 310 315 320
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 325 330 335
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 340 345 350
 Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
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 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
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 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 385 390 395 400
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 405 410 415
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 420 425 430
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
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<220>
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28

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mgnacngtnw sncsnwsnws naarsnccn tggtngarw sngartayyt ngaytaytn 360
ttygargtng arccngcncc nccngtnytn gtnynacnc aracngarga rathytnwsn 420
gcnaaycna cntaycaryt nccnccntgy atgccnccny tngayytnaa rtaygargtn 480
gcnttytgga argarggngc nggnaayaar acnytnttyc cngtnacncc ncayggncar 540
ccngtncara thacnytnca rccngcngcn wsngarcayc aytgyytnws ncgnmgnacn 600
athtayacnt tywsngtncc naartaywsn aarttywsna arccnacntg ytttytyn 660
gargtnccng argcnaaytg ggcnttyytn gtnytnccnw snytnytnat hytnytnytn 720
gtnathgcng cnggnggngt nathtggaar acnytnatgg gnaayccntg gttycarmgn 780
gcnaaratgc cmgngcnnyt ngaytaywsn ggnacayacnc aycngtngc nacnttycar 840
ccnwsnmgnnc cngarwsngt naaygayyt tyytntgyc cncaraarga rytnacnmgn 900
ggngtnmgnc cnacnccnmg ngtmgnacn ccngcnacnc arcaraacnmg ntggaaraar 960
gavytngcng argaygarga rgargargay gargargaya cngargaygg ngtnwsntty 1020
carccntaya thgarccncc nwsnttaytn ggnacargarc aycargcncc nggnacaywsn 1080
gargcnggng gngtngayws nggnmgnccn mgngcnccny tngtnccnws ngarggnwsn 1140
wsngcntggg aywsnwsnga ymgnwsntgg gcnwsnacng tngaywsnws ntggaymgn 1200
gnggnwsnw snggntayyt ncngaraar ggnccnggnc arggnccngg ngngayggn 1260
caycargarw snytnccncc nccngartty wsnaargayw snggnttayt ngargarytn 1320
ccngargaya ayytnwsnws ntggcnacn tgggnacny tnccnccnra rccnaayyt 1380
gtnccnggng gnccnccngt nwsnytnca acnytnacnt tytgytggga rwsnwsnccn 1440
gargargarg argargcnmg ngarwsngar athgargayw sngaygcngg nwsntgggn 1500
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<210> 29

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

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<221> misc feature

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<223> n = A,T,C or G

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ytnacnttgg tncnccngnyt nggnaayccn cargaygtnta cntayttygt ncntaycar	180
wsnwsnccna cnmgnmgnmg ntggmgnar gtngargart gycnggnac naargarytn	240
ytnytnwsna tgatgtgyt naaraarcar gayytn taya ayaartt yaa rggnmgn gtn	300
mgna cngt nw sncnwsnws naarwsnccn tgggtngarw sngartayyt ngaytayyt n	360
ttygargtng arccngcncc nccnctn ytn gtnytnacnc aracngarga rathytnwsn	420
gcnaaygcna cntaycaryt nccnccntgy atgcccncn ytn gayytnaa rtayqargt n	480

gcnttytgga argarggngc nggnaayaar gtnggnwsnw snttyccngc nccnmgnyn	540
ggnccnnytny tncayccntt yytnytnmgn ttyttywsnc cnwsncarcc ngcncncn	600
ccnnytnytnc argargtntt yccngtncay wsn	633

<210> 30
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide Primer ZC39204

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ccag	64

<210> 31
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<210> 32
 <211> 1922
 <212> DNA
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<220>
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<221> CDS
 <222> (123)...(1922)

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caggaaacag ccagtccgtt taggttttt cacgagcaact tcaccaacaa ggaccataga	120

tt atg aaa act gaa gaa ggt aaa ctg gta atc tgg att aac ggc gat			167
Met Lys Thr Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp			
1	5	10	15
aaa ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat			215
Lys Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp			
20	25	30	
acc gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa			263
Thr Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys			
35	40	45	
ttc cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg			311
Phe Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp			
50	55	60	
gca cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa			359
Ala His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu			
65	70	75	
atc acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg			407
Ile Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp			
80	85	90	95
gat gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt			455
Asp Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val			
100	105	110	
gaa gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca			503
Glu Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro			
115	120	125	
aaa acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa			551
Lys Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys			
130	135	140	
ggt aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg			599
Gly Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp			
145	150	155	
ccg ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc			647
Pro Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly			
160	165	170	175

aag tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg Lys Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala 180 185 190	695
ggt ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca Gly Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala 195 200 205	743
gac acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr 210 215 220	791
gcg atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc Ala Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser 225 230 235	839
aaa gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro 240 245 250 255	887
tcc aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser 260 265 270	935
ccg aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr 275 280 285	983
gat gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val 290 295 300	1031
gcg ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala 305 310 315	1079
gcc acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro 320 325 330 335	1127
cag atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc	1175

Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala	340	345	350	
gcc agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act				1223
Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr	355	360	365	
aat tcg agc tcc cac cat cac cat cac gcg aat tcg gta ccg ctg				1271
Asn Ser Ser His His His His His Ala Asn Ser Val Pro Leu	370	375	380	
gtt ccg cgt gga tcc agg ccc cgt ctg gcc cct ccc cag aat gtg acg				1319
Val Pro Arg Gly Ser Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr	385	390	395	
ctg ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt				1367
Leu Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu	400	405	410	415
ggc aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc				1415
Gly Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro	420	425	430	
acc cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag				1463
Thr Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu	435	440	445	
ctg cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag				1511
Leu Leu Cys Ser Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys	450	455	460	
ttc aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg				1559
Phe Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp	465	470	475	
gtg gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca				1607
Val Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro	480	485	490	495
cct gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc				1655
Pro Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala	500	505	510	

acg tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag	515	520	525	1703
Thr Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu				
gtg gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc	530	535	540	1751
Val Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val				
act ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc	545	550	555	1799
Thr Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser				
gaa cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg	560	565	570	1847
Glu His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro				
aaa tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca	580	585	590	1895
Lys Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro				
gaa gcc aac tgg tgt ttt ggc gga tga	595			1922
Glu Ala Asn Trp Cys Phe Gly Gly *				
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Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe	35	40	45	
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala	50	55	60	

His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
 65 70 75 80
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
 85 90 95
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
 100 105 110
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
 115 120 125
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
 130 135 140
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
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<210> 34
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Asn Phe Ser Val .
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<400> 36
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<210> 37
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<210> 38
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cccttcctgc tccttgact gcgt	24
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<220>	
<223> 01igonucleotide primer ZC39408	
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<400> 47

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<210> 48

<211> 25

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<400> 48

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<210> 49

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<400> 49

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